AMENDMENTS TO THE SPECIFICATION

Please amend the Specification as indicated in the replacement paragraph below.

In the specification:

Please amend the paragraph as presented at page 36, line 4 to page 37, line 13 of

the Specification as originally filed, as follows:

FIG. 3 is a set of diagrams showing the construction of full-length JEV cDNA clones in bacterial artificial chromosome (BAC) pBeloBAC11. (A) A schematic diagram of the full-length JEV cDNAs constructed in pBeloBAC11. Viral proteins are shown with thick solid lines at both termini representing the 5' and 3' NTRs of the viral genome. The SP6 and T7 promoter transcription start sites and the unique restriction endonuclease recognition site ensuring runoff transcription are shown at the 5' and 3' ends, respectively. (B-C) A set of schematic diagrams showing the 5' and 3' termini of full-length JEV cDNA clones. Nucleotide sequences of JEV genomic RNA are shown as bold italic lowercase letters. Illustrated are the 5' termini of four SP6-driven (B) and four T7-driven (C) full-length JEV cDNA templates (SEQ. ID. No: 68). To produce SP6 and T7 RNA polymerase runoff products, the 3' termini of two SP6-driven (B, pBAC^{SP6}/JVFL/*Xho*I and pBAC^{SP6}/JVFLx/*Xho*I) and two T7-driven (C, pBAC^{T7}/JVFL/*Xho*I and pBAC^{T7}/JVFLx/*Xho*I) JEV cDNA templates were linearized by *Xho* I digestion (SEQ. ID. No: 69), resulting in three nucleotides (CGA) of virus-unrelated sequence at the 3' ends. Similarly, the cutting of the 3' termini of an SP6-driven (B, pBAC^{SP6}/JVFLx/*Xba*I) and a T7-driven (C, pBAC^{T7}/JVFLx/*Xba*I) JEV cDNA template with *Xba* I resulted in four nucleotides (CTAG) of virus-unrelated sequence at the 3' ends (SEQ. ID. NO: 70). In contrast, the authentic 3' end of JEV genomic RNA was present when SP6-driven (B, pBAC^{SP6}/JVFLx/*Xba*I^{MBN}) and T7-driven (C, pBAC^{T7}/JVFLx/*Xba*I^{MBN}) JEV cDNA templates were linearized by *Xba* I digestion and then treated with mung bean nuclease (MBN) to remove the unrelated single-stranded sequences (SEQ. ID. No: 71). Underlined is the restriction endonuclease recognition site introduced at the 3' end of the viral genome. An arrowhead indicates a cleavage site.

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AMENDMENT TO THE SEQUENCE LISTING

In the Sequence Listing:

Please substitute the originally filed Sequence Listing with the ninety-five (95) pages of substitute sheets for the amendment to the Sequence Listing and computer readable copy of the sequence listing, as attached hereto.